



1600

## RAW SEQUENCE LISTING

DATE: 08/14/2003

PATENT APPLICATION: US/09/834,792C

TIME: 15:04:01

Input Set : A:\pto.da.txt

Output Set: N:\CRF4\08142003\I834792C.raw

3 <110> APPLICANT: Mount Sinai School of Medicine of NYU  
 5 <120> TITLE OF INVENTION: TRP8, A TRANSIENT RECEPTOR POTENTIAL  
 6 CHANNEL EXPRESSED IN TASTE RECEPTOR CELL  
 9 <130> FILE REFERENCE: 1270-007  
 11 <140> CURRENT APPLICATION NUMBER: 09/834,792C  
 12 <141> CURRENT FILING DATE: 2001-04-13  
 14 <150> PRIOR APPLICATION NUMBER: 60/197,491  
 15 <151> PRIOR FILING DATE: 2000-04-17  
 17 <160> NUMBER OF SEQ ID NOS: 4  
 19 <170> SOFTWARE: Windows 2000 MS DOS w/ line breaks

## ERRORED SEQUENCES

*Ad*  
 Does Not Comply  
 Corrected Diskette Needed

326 <210> SEQ ID NO: 4  
 327 <211> LENGTH: 1165  
 328 <212> TYPE: PRT  
 329 <213> ORGANISM: Human  
 331 <400> SEQUENCE: 4  
 332 Met Gln Asp Val Gln Gly Pro Arg Pro Gly Ser Pro Gly Asp Ala Glu  
 333 1 5 10 15  
 334 Asp Arg Arg Glu Leu Gly Leu His Arg Gly Glu Val Asn Phe Gly Gly  
 335 20 25 30  
 336 Ser Gly Lys Lys Arg Gly Lys Phe Val Arg Val Pro Ser Gly Val Ala  
 337 35 40 45  
 338 Pro Ser Val Leu Phe Asp Leu Leu Ala Glu Trp His Leu Pro Ala  
 339 50 55 60  
 340 Pro Asn Leu Val Val Ser Leu Val Gly Glu Glu Gln Pro Phe Ala Met  
 341 65 70 75 80  
 342 Lys Ser Trp Leu Arg Asp Val Leu Arg Lys Gly Leu Val Lys Ala Ala  
 343 85 90 95  
 344 Gln Ser Thr Gly Ala Trp Ile Leu Thr Ser Ala Leu Arg Val Gly Leu  
 345 100 105 110  
 346 Ala Arg His Val Gly Gln Ala Val Arg Asp His Ser Leu Ala Ser Thr  
 347 115 120 125  
 349 Ser Thr Lys Val Arg Val Val Ala Val Gly Met Ala Ser Leu Gly Arg  
 350 130 135 140  
 351 Val Leu His Arg Arg Ile Leu Glu Glu Ala Gln Glu Asp Phe Pro Val  
 352 145 150 155 160  
 353 His Tyr Pro Glu Asp Asp Gly Gly Ser Gln Gly Pro Leu Cys Ser Leu  
 354 165 170 175  
 355 Asp Ser Asn Leu Ser His Phe Ile Leu Val Glu Pro Gly Pro Pro Gly  
 356 180 185 190

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```

357 Lys Gly Asp Gly Leu Thr Glu Leu Arg Leu Arg Leu Glu Lys His Ile
358          195          200          205
359 Ser Glu Gln Arg Ala Gly Tyr Gly Gly Thr Gly Ser Ile Glu Ile Pro
360      210          215          220
361 Val Leu Cys Leu Leu Val Asn Gly Asp Pro Asn Thr Leu Glu Arg Ile
362 225          230          235          240
363 Ser Arg Ala Val Glu Gln Ala Ala Pro Trp Leu Ile Leu Val Gly Ser
364          245          250          255
365 Gly Gly Ile Ala Asp Val Leu Ala Ala Leu Val Asn Gln Pro His Leu
366          260          265          270
367 Leu Val Pro Lys Val Ala Glu Lys Gln Phe Lys Glu Lys Phe Pro Ser
368          275          280          285
369 Lys His Phe Ser Trp Glu Asp Ile Val Arg Trp Thr Lys Leu Leu Gln
370      290          295          300
371 Asn Ile Thr Ser His Gln His Leu Leu Thr Val Tyr Asp Phe Glu Gln
372 305          310          315          320
373 Glu Gly Ser Glu Glu Leu Asp Thr Val Ile Leu Lys Ala Leu Val Lys
374          325          330          335
375 Ala Cys Lys Ser His Ser Gln Glu Pro Gln Asp Tyr Leu Asp Glu Leu
376          340          345          350
377 Lys Leu Ala Val Ala Trp Asp Arg Val Asp Ile Ala Lys Ser Glu Ile
378          355          360          365
379 Phe Asn Gly Asp Val Glu Trp Lys Ser Cys Asp Leu Glu Glu Val Met
380      370          375          380
381 Val Asp Ala Leu Val Ser Asn Lys Pro Glu Phe Val Arg Leu Phe Val
382 385          390          395          400
383 Asp Asn Gly Ala Asp Val Ala Asp Phe Leu Thr Tyr Gly Arg Leu Gln
384          405          410          415
385 Glu Leu Tyr Arg Ser Val Ser Arg Lys Ser Leu Leu Phe Asp Leu Leu
386          420          425          430
387 Gln Arg Lys Gln Glu Glu Ala Arg Leu Thr Leu Ala Gly Leu Gly Thr
388          435          440          445
389 Gln Gln Ala Arg Glu Pro Pro Ala Gly Pro Pro Ala Phe Ser Leu His
390      450          455          460
391 Glu Val Ser Arg Val Leu Lys Asp Phe Leu Gln Asp Ala Cys Arg Gly
393 465          470          475          480
394 Phe Tyr Gln Asp Gly Arg Pro Gly Asp Arg Arg Arg Ala Glu Lys Gly
395          485          490          495
396 Pro Ala Lys Arg Pro Thr Gly Gln Lys Trp Leu Leu Asp Leu Asn Gln
397          500          505          510
398 Lys Ser Glu Asn Pro Trp Arg Asp Leu Phe Leu Trp Ala Val Leu Gln
399          515          520          525
400 Asn Arg His Glu Met Ala Thr Tyr Phe Trp Ala Met Gly Gln Glu Gly
401      530          535          540
402 Val Ala Ala Ala Leu Ala Ala Cys Lys Ile Leu Lys Glu Met Ser His
403 545          550          555          560
404 Leu Glu Thr Glu Ala Glu Ala Ala Arg Ala Thr Arg Glu Ala Lys Tyr
405          565          570          575
406 Glu Arg Leu Ala Leu Asp Leu Phe Ser Glu Cys Tyr Ser Asn Ser Glu

```

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```

407          580          585          590
408 Ala Arg Ala Phe Ala Leu Leu Val Arg Arg Asn Arg Cys Trp Ser Lys
409          595          600          605
410 Thr Thr Cys Leu His Leu Ala Thr Glu Ala Asp Ala Lys Ala Phe Phe
411          610          615          620
412 Ala His Asp Gly Val Gln Ala Phe Leu Thr Arg Ile Trp Trp Gly Asp
413 625          630          635          640
414 Met Ala Ala Gly Thr Pro Ile Leu Arg Leu Leu Gly Ala Phe Leu Cys
415          645          650          655
416 Phe Ala Leu Val Tyr Thr Asn Leu Ile Thr Phe Ser Glu Glu Ala Pro
417          660          665          670
418 Leu Arg Thr Gly Leu Glu Asp Leu Gln Asp Leu Asp Ser Leu Asp Thr
419          675          680          685
420 Glu Lys Ser Pro Leu Tyr Gly Leu Gln Ser Arg Val Glu Glu Leu Val
421          690          695          700
422 Glu Ala Pro Arg Ala Gln Gly Asp Arg Gly Pro Arg Ala Val Phe Leu
423 705          710          715          720
424 Leu Thr Arg Trp Arg Lys Phe Trp Gly Ala Pro Val Thr Val Phe Leu
425          725          730          735
426 Gly Asn Val Val Met Tyr Phe Ala Phe Leu Phe Leu Phe Thr Tyr Val
427          740          745          750
428 Leu Leu Val Asp Phe Arg Pro Pro Pro Gln Gly Pro Ser Gly Pro Glu
429          755          760          765
430 Val Thr Leu Tyr Phe Trp Val Phe Thr Leu Val Leu Glu Glu Ile Arg
431          770          775          780
432 Gln Gly Phe Phe Thr Asp Glu Asp Thr His Leu Val Lys Lys Phe Thr
433 785          790          795          800
434 Leu Tyr Val Gly Asp Asn Trp Asn Lys Cys Asp Met Val Ala Ile Phe
435          805          810          815
436 Leu Phe Ile Val Gly Val Thr Cys Arg Met Leu Pro Ser Ala Phe Glu
437          820          825          830
438 Ala Gly Arg Thr Val Leu Ala Met Asp Phe Met Val Phe Thr Leu Arg
439          835          840          845
440 Leu Ile His Ile Phe Ala Ile His Lys Gln Leu Gly Pro Lys Ile Ile
441          850          855          860
442 Val Val Glu Arg Met Met Lys Asp Val Phe Phe Phe Leu Phe Phe Leu
443 865          870          875          880
444 Ser Val Trp Leu Val Ala Tyr Gly Val Thr Thr Gln Ala Leu Leu His
445          885          890          895
446 Pro His Asp Gly Arg Leu Glu Trp Ile Phe Arg Arg Val Leu Tyr Arg
447          900          905          910
448 Pro Tyr Leu Gln Ile Phe Gly Gln Ile Pro Leu Asp Glu Ile Asp Glu
449          915          920          925
450 Ala Arg Val Asn Cys Ser Thr His Pro Leu Leu Leu Glu Asp Ser Pro
451          930          935          940
452 Ser Cys Pro Ser Leu Tyr Ala Asn Trp Leu Val Ile Leu Leu Leu Val
453 945          950          955          960
454 Thr Phe Leu Leu Val Thr Asn Val Leu Leu Met Asn Leu Leu Ile Ala
455          965          970          975

```

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```

456 Met Phe Ser Tyr Thr Phe Gln Val Val Gln Gly Asn Ala Thr Met Phe
457          980          985          990
458 Trp Lys Phe Gln Arg Tyr Asn Leu Ile Val Glu Tyr His Glu Arg Pro
459          995          1000          1005
460 Ala Leu Ala Pro Pro Phe Ile Leu Leu Ser His Leu Ser Leu Thr Leu
461          1010          1015          1020
462 Arg Arg Val Phe Lys Lys Glu Ala Glu His Lys Arg Glu His Leu Glu
463 1025          1030          1035          1040
464 Arg Asp Leu Pro Asp Pro Leu Asp Gln Lys Val Val Thr Trp Glu Thr
465          1045          1050          1055
466 Val Gln Lys Glu Asn Phe Leu Ser Lys Met Glu Lys Arg Arg Arg Asp
467          1060          1065          1070
468 Ser Glu Gly Glu Val Leu Arg Lys Thr Ala His Arg Val Asp Phe Ile
469          1075          1080          1085
470 Ala Lys Tyr Leu Gly Gly Leu Arg Glu Gln Glu Lys Arg Ile Lys Cys
471          1090          1095          1100
472 Leu Glu Ser Gln Ile Asn Tyr Cys Ser Val Leu Val Ser Ser Val Ala
473 1105          1110          1115          1120
474 Asp Val Leu Ala Gln Gly Gly Gly Pro Arg Ser Ser Gln His Cys Gly
475          1125          1130          1135
476 Glu Gly Ser Gln Leu Val Ala Ala Asp His Arg Gly Gly Ile Asp Gly
477          1140          1145          1150
478 Trp Glu Gln Pro Gly Ala Gly Gln Pro Pro Ser Asp Thr
479          1155          1160          1165
E--> 496 1P

```

VERIFICATION SUMMARY

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TIME: 15:04:02

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Output Set: N:\CRF4\08142003\I834792C.raw

L:496 M:332 E: (32) Invalid/Missing Amino Acid Numbering, SEQ ID:4